#2

OIPE

RAW SEQUENCE LISTING   DATE: 12/05/2001
PATENT APPLICATION: US/09/993,180   TIME: 11:53:53

ENTERED

Input Set : A:\es.txt
Output Set: N:\CRF3\11212001\I993180.raw

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      3 <110> APPLICANT: Bristol-Myers Squibb Company
      5 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN SERPIN SECRETED FROM
LYMPHOID
      6        CELLS, LSI-01
      8 <130> FILE REFERENCE: D0051.NP
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/993,180
C--> 10 <141> CURRENT FILING DATE: 2001-11-14
     10 <150> PRIOR APPLICATION NUMBER: US 60/248,434
     11 <151> PRIOR FILING DATE: 2000-11-14
     13 <150> PRIOR APPLICATION NUMBER: US 60/257,610
     14 <151> PRIOR FILING DATE: 2000-12-21
     16 <150> PRIOR APPLICATION NUMBER: US 60/282,745
     17 <151> PRIOR FILING DATE: 2001-04-10
     19 <160> NUMBER OF SEQ ID NOS: 46
     21 <170> SOFTWARE: PatentIn version 3.0
     23 <210> SEQ ID NO: 1
     24 <211> LENGTH: 1766
     25 <212> TYPE: DNA
     26 <213> ORGANISM: Homo sapiens
     28 <220> FEATURE:
     29 <221> NAME/KEY: CDS
     30 <222> LOCATION: (68)..(1372)
     32 <400> SEQUENCE: 1
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     35 accaacc atg caa gga cag ggc agg aga aga gga acc tgc aaa gac ata       109
     36         Met Gln Gly Gln Gly Arg Arg Arg Gly Thr Cys Lys Asp Ile
     37         1               5                   10
     39 ttt tgt tcc aaa atg gca tct tac ctt tat gga gta ctc ttt gct gtt      157
     40 Phe Cys Ser Lys Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val
     41 15              20                  25                  30
     43 ggc ctc tgt gct cca atc tac tgt gtg tcc ccg gcc aat gcc ccc agt      205
     44 Gly Leu Cys Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser
     45             35                  40                  45
     47 gca tac ccc cgc cct tcc tcc aca aag agc acc cct gcc tca cag gtg      253
     48 Ala Tyr Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val
     49             50                  55                  60
     51 tat tcc ctc aac acc gac ttt gcc ttc cgc cta tac cgc agg ctg gtt      301
     52 Tyr Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
     53             65                  70                  75
     55 ttg gag acc ccg agt cag aac atc ttc ttc tcc cct gtg agt gtc tcc      349
     56 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val Ser
     57      80                  85                  90
     59 act tcc ctg gcc atg ctc tcc ctt ggg gcc cac tca gtc acc aag acc      397
     60 Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr Lys Thr
     61 95                  100                 105                 110
     63 cag att ctc cag ggc ctg ggc ttc aac ctc aca cac aca cca gag tct      445
     64 Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr Pro Glu Ser
     65                 115                 120                 125
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67 gcc atc cac cag ggc ttc cag cac ctg gtt cac tca ctg act gtt ccc      493
68 Ala Ile His Gln Gly Phe Gln His Leu Val His Ser Leu Thr Val Pro
69             130             135             140
71 agc aaa gac ctg acc ttg aag atg gga agt gcc ctc ttc gtc aag aag      541
72 Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala Leu Phe Val Lys Lys
73             145             150             155
75 gag ctg cag ctg cag gca aat ttc ttg ggc aat gtc aag agg ctg tat      589
76 Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly Asn Val Lys Arg Leu Tyr
77       160             165             170
79 gaa gca gaa gtc ttt tct aca gat ttc tcc aac ccc tcc att gcc cag      637
80 Glu Ala Glu Val Phe Ser Thr Asp Phe Ser Asn Pro Ser Ile Ala Gln
81 175             180             185             190
83 gcg agg atc aac agc cat gtg aaa aag aag acc caa ggg aag gtt gta      685
84 Ala Arg Ile Asn Ser His Val Lys Lys Lys Thr Gln Gly Lys Val Val
85             195             200             205
87 gac ata atc caa ggc ctt gac ctt ctg acg gcc atg gtt ctg gtg aat      733
88 Asp Ile Ile Gln Gly Leu Asp Leu Leu Thr Ala Met Val Leu Val Asn
89             210             215             220
91 cac att ttc ttt aaa gcc aag tgg gag aag ccc ttt cac ctt gaa tat      781
92 His Ile Phe Phe Lys Ala Lys Trp Glu Lys Pro Phe His Leu Glu Tyr
93             225             230             235
95 aca aga aag aac ttc cca ttc ctg gtg ggc gag cag gtc act gtg caa      829
96 Thr Arg Lys Asn Phe Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln
97       240             245             250
99 gtc ccc atg atg cac cag aaa gag cag ttc gct ttt ggg gtg gat aca      877
100 Val Pro Met Met His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr
101 255             260             265             270
103 gag ctg aac tgc ttt gtg ctg cag atg gat tac aag gga gat gcc gtg     925
104 Glu Leu Asn Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val
105             275             280             285
107 gcc ttc ttt gtc ctc cct agc aag ggc aag atg agg caa ctg gaa cag     973
108 Ala Phe Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln
109             290             295             300
111 gcc ttg tca gcc aga aca ctg ata aag tgg agc cac tca ctc cag aaa     1021
112 Ala Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys
113       305             310             315
115 agg tgg ata gag gtg ttc atc ccc aga ttt tcc att tct gcc tcc tac     1069
116 Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser Tyr
117       320             325             330
119 aat ctg gaa acc atc ctc ccg aag atg ggc atc caa aat gcc ttt gac     1117
120 Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala Phe Asp
121 335             340             345             350
123 aaa aat gct gat ttt tct gga att gca aag aga gac tcc ctg cag gtt     1165
124 Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser Leu Gln Val
125             355             360             365
127 tct aaa gca acc cac aag gct gtg ctg gat gtc agt gaa gag ggc act     1213
128 Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser Glu Glu Gly Thr
129             370             375             380
131 gag gcc aca gca gct acc acc acc aag ttc ata gtc cga tcg aag gat     1261
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132 Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile Val Arg Ser Lys Asp
133         385             390             395
135 ggt ccc tct tac ttc act gtc tcc ttc aat agg acc ttc ctg atg atg    1309
136 Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn Arg Thr Phe Leu Met Met
137         400             405             410
139 att aca aat aaa gcc aca gac ggt att ctc ttt cta ggg aaa gtg gaa    1357
140 Ile Thr Asn Lys Ala Thr Asp Gly Ile Leu Phe Leu Gly Lys Val Glu
141 415             420             425             430
143 aat ccc act aaa tcc taggtgggaa atggcctgtt aactgatggc acattgctaa    1412
144 Asn Pro Thr Lys Ser
145             435
147 tgcacaagaa ataacaaacc acatccctct ttctgttctg agggtgcatt tgaccccagt    1472
149 ggagctggat tcgctggcag ggatgccact tccaaggctc aatcaccaaa ccatcaacag    1532
151 ggaccccagt cacaagccaa cacccattaa ccccagtcag tgcccttttc cacaaattct    1592
153 cccaggtaac tagcttcatg ggatgttgct gggttaccat atttccattc cttggggctc    1652
155 ccaggaatgg aaatacgcca acccaggtta ggcacctcta ttgcagaatt acaataacac    1712
157 attcaataaa actaaaatat gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa           1766
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 435
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
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167 Met Gln Gly Gln Gly Arg Arg Arg Gly Thr Cys Lys Asp Ile Phe Cys
168 1               5               10              15
171 Ser Lys Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu
172             20              25              30
175 Cys Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr
176             35              40              45
179 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr Ser
180         50              55              60
183 Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val Leu Glu
184 65              70              75              80
187 Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val Ser Thr Ser
188             85              90              95
191 Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr Lys Thr Gln Ile
192             100             105             110
195 Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr Pro Glu Ser Ala Ile
196         115             120             125
199 His Gln Gly Phe Gln His Leu Val His Ser Leu Thr Val Pro Ser Lys
200         130             135             140
203 Asp Leu Thr Leu Lys Met Gly Ser Ala Leu Phe Val Lys Lys Glu Leu
204 145             150             155             160
207 Gln Leu Gln Ala Asn Phe Leu Gly Asn Val Lys Arg Leu Tyr Glu Ala
208             165             170             175
211 Glu Val Phe Ser Thr Asp Phe Ser Asn Pro Ser Ile Ala Gln Ala Arg
212             180             185             190
215 Ile Asn Ser His Val Lys Lys Lys Thr Gln Gly Lys Val Val Asp Ile
216         195             200             205
219 Ile Gln Gly Leu Asp Leu Leu Thr Ala Met Val Leu Val Asn His Ile
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220      210                    215                    220
 223 Phe Phe Lys Ala Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg
 224 225                    230                    235                    240
 227 Lys Asn Phe Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro
 228                    245                    250                    255
 231 Met Met His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu
 232                    260                    265                    270
 235 Asn Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe
 236            275                    280                    285
 239 Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala Leu
 240      290                    295                    300
 243 Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys Arg Trp
 244 305                    310                    315                    320
 247 Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser Tyr Asn Leu
 248                    325                    330                    335
 251 Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala Phe Asp Lys Asn
 252            340                    345                    350
 255 Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser Leu Gln Val Ser Lys
 256            355                    360                    365
 259 Ala Thr His Lys Ala Val Leu Asp Val Ser Glu Glu Gly Thr Glu Ala
 260      370                    375                    380
 263 Thr Ala Ala Thr Thr Thr Lys Phe Ile Val Arg Ser Lys Asp Gly Pro
 264 385                    390                    395                    400
 267 Ser Tyr Phe Thr Val Ser Phe Asn Arg Thr Phe Leu Met Met Ile Thr
 268                    405                    410                    415
 271 Asn Lys Ala Thr Asp Gly Ile Leu Phe Leu Gly Lys Val Glu Asn Pro
 272            420                    425                    430
 275 Thr Lys Ser
 276            435
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279 <210> SEQ ID NO: 3
280 <211> LENGTH: 423
281 <212> TYPE: PRT
282 <213> ORGANISM: Homo sapiens

284 <400> SEQUENCE: 3

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287 1                    5                    10                    15
289 Phe Cys Pro Ala Val Leu Cys His Pro Asn Ser Pro Leu Asp Glu Glu
290            20                    25                    30
292 Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr His Val Asp Leu Gly
293            35                    40                    45
295 Leu Ala Ser Ala Asn Val Asp Phe Ala Phe Ser Leu Tyr Lys Gln Leu
296      50                    55                    60
298 Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe Ser Pro Leu Ser Ile
299 65                    70                    75                    80
301 Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala His Asn Thr Thr Leu
302            85                    90                    95
304 Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu Thr Glu Thr Ser Glu
305            100                    105                    110
307 Ala Glu Ile His Gln Ser Phe Gln His Leu Leu Arg Thr Leu Asn Gln
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Input Set : A:\es.txt
Output Set: N:\CRF3\11212001\I993180.raw

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308           115              120              125
310 Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn Ala Met Phe Val Lys
311      130              135              140
313 Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu Asp Ala Lys Arg Leu
314 145              150              155              160
316 Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln Asp Ser Ala Ala Ala
317              165              170              175
319 Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly Thr Arg Gly Lys Ile
320              180              185              190
322 Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr Met Met Val Leu Val
323      195              200              205
325 Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met Pro Phe Asp Pro Gln
326      210              215              220
328 Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys Lys Lys Trp Val Met
329 225              230              235              240
331 Val Pro Met Met Ser Leu His His Leu Thr Ile Pro Tyr Phe Arg Asp
332              245              250              255
334 Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys Tyr Thr Gly Asn Ala
335              260              265              270
337 Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys Met Glu Glu Val Glu
338      275              280.             285
340 Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp Arg Asp Ser Leu Glu
341      290              295              300
343 Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys Phe Ser Ile Ser Arg
344 305              310              315              320
346 Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu Gly Ile Glu Glu Ala
347              325              330              335
349 Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr Gly Ala Arg Asn Leu
350      340              345              350
352 Ala Val Ser Gln Val Val His Lys Ala Val Leu Asp Val Phe Glu Glu
353      355              360              365
355 Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys Ile Thr Leu Leu Ser
356      370              375              380
358 Ala Leu Val Glu Thr Arg Thr Ile Val Arg Phe Asn Arg Pro Phe Leu
359 385              390              395              400
361 Met Ile Ile Val Pro Thr Asp Thr Gln Asn Ile Phe Phe Met Ser Lys
362              405              410              415
364 Val Thr Asn Pro Lys Gln Ala
365              420
367 <210> SEQ ID NO: 4
368 <211> LENGTH: 427
369 <212> TYPE: PRT
370 <213> ORGANISM: Homo sapiens
372 <400> SEQUENCE: 4
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377 Leu Ser His Gly Gln Leu His Val Glu His Asp Gly Glu Ser Cys Ser
378              20               25 ·             30
380 Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser
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VERIFICATION SUMMARY   DATE: 12/05/2001
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Input Set : **A:\es.txt**
Output Set: **N:\CRF3\11212001\I993180.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date